

Figure 6. Four ATPase subfamilies: Signatures of SNF2, ISWI, CHD, and Ino80. The grouping of the remodeling ATPase of the Snf2 family is defined by signature motifs within the ATPase domain, whereas additional domains define the subfamilies. Members of the INO80 (and Swr1) subfamily of ATPases have a longer insertion between the two ATPase subdomains than other remodelers (Fig. 5). These subfamilies also contain a HSA (helicase-SANT) domain. The SWI/SNF family of ATPases contains a HSA domain, but is further defined by a carboxy-terminal bromodomain (capable of binding acetylated lysine residues). The ISWI and CHD family of ATPases each have SANT-SLIDE modules (blue) whereas only the CHD family has tandem chromodomains. (Adapted, with permission, from Clapier and Cairns 2009, © Annual Reviews.)

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